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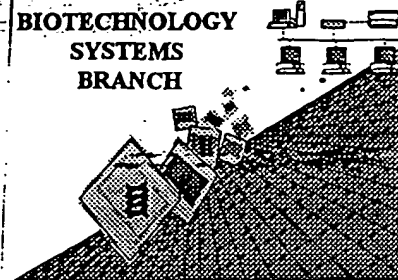
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K. Conalla

RAW SEQUENCE LISTING **ERROR REPORT**



p#12

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/373,658 A

Source: 1642

Date Processed by STIC: 11-20-00

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/373,658A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☒ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) _____ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

Canela

1642

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/373,658A DATE: 11/20/2000
 TIME: 16:02:55

Input Set : A:\seqlist14881070006.txt
 Output Set: N:\CRF3\11202000\I373658A.raw

Does Not Comply
 Corrected Diskette Needed

see pp. 1, 2

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TECH CENTER 1800/2900

7 <110> APPLICANT: Iruela-Arispe, Luisa
 10 Hastings, Gregg A.
 13 Ruben, Steven M.
 16 Jonak, Zdenka L.
 19 Trulli, Stephen H.
 22 Fronwald, James A.
 25 Terrett, Jonathan A.
 31 <120> TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
 37 <130> FILE REFERENCE: 1488.1070006
 43 <140> CURRENT APPLICATION NUMBER: 09/373,658A
 47 <141> CURRENT FILING DATE: 1999-08-13
 54 <160> NUMBER OF SEQ ID NOS: 127
 60 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORRED SEQUENCES

37488 <210> SEQ ID NO: 95
 37491 <211> LENGTH: 716
 E--> 37494 <212> TYPE: CDNA
 37497 <213> ORGANISM: Homo sapiens
 37503 <400> SEQUENCE: 95
 37506 taagtttgc agtcctttgc aaacagactg acgctgagtg tccgtgtctga gtcaataagt 60
 37509 gcacttttac cttttaacct atgccctcta cttgaaccgg agcaagggtcc agtcactgg 120
 37512 acagttgatg ataggggtctg ccgccccata cccctccttc tccccctta ggaatttgtg 180
 37515 cagtactgga ggggttgcyg caatgggagc octygggtgg cgtgctgccc ttgatattgg 240
 37518 caagggagccc agtcaccaca gtggagagccc ttgtctgcac ctcagtaccg catgtccagg 300
 37521 agcacaagac tggccccctgc ccccttgaat cacagggggc acagctggcl ttcgcagggc 360
 37524 ttggcatcct cgggtttcag agccttgttg caggtggcag aggcctggcc ggaggggtcc 420
 37527 ctgcactcta cagttcgctt ctgccagccg gccccgcagg tgctagagca ctccagaccg 480
 37530 tccccagca cccactgtgc gtygagcagc ggcctggatga tgttgggtgt tgcctctctt 540
 37533 ttgtgtctct gcatgctaaa agtcacgtca ttaygaanca aagaagggtgt atttgacttt 600
 37536 ttggggggaa gaacctcgcc caggactgtc aggaagctyca ctgtcagaag gctctgcnaa 660
 37539 ggcccnagaag ctctgcagcc gctccagggt ggcgatggag ccgtgtactt caggat 716

Valid responses for <212> are:

- DNA
 - RNA
 - PRT

US 09/373,658A

P.2

<210> 94 Seq # 94

<211> 652

<212> DNA

<213> Homo sapiens

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TECH CENTER 1600/2800

<400> 94

→ missing mandatory <220> to <223>
features to explain "n" at location
524. See #10 on Error Summary

Sheet

ggcataagat cacacttttag ttcagagaca catttgata aatacttgaa atggatccac 60
ccctgcaggt ggcagcctga gaacatggcg ctgcaggggg accagggcag cgtctggttc 120
aggtggacga acagcgggtgc catcacgtgg tgcttgccca tgggcccga gagccgtgtg 180
cagggcttgg agtcgtcgtg gggcatgctg aggacgtgcc ctagtccatg ggccaggggtg 240
tgggcccgcct ggagcccctc atcctcgatc acggagcagc ttttggtggg gtcacaaatg 300
gtcccgatgt ctgccacacc caggggtgtca cacagcccct cctgccaca gaagttctgt 360
ctggtgagca ggatggccgt gtcgtagtgc tctgggtggc ggtcgtctgg ctggttgaaa 420
cgccgctgcc agttgcagaa gttacgcagt gtaagcccc cattgtcgga cacctctggg 480
ccccattttt catctttctac gatcagcact tttaccacca t^ocagttgat ggaattcttg 540
atgctggggg gcttgtagaa tcgggcttgc cacgaaaatt aacctcagga tgtggttctg 600
caggtcggcc cgtaaagggc gccatggacg catcgccac caacagcgtt tc 652

← This error is indicated elsewhere
in the sequence listing. Please check
entire sequence listing for "n's" and "Xaa's"
and ensure that an explanation is presented in the <220> to <223>
features.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/373,658A

DATE: 11/20/2000

TIME: 16:02:58

Input Set : A:\seqlist14881070006.txt

Output Set: N:\CRF3\11202000\I373658A.raw

L:889 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:907 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:2250 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:2256 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:4453 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:4489 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:4495 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:4501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:4752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:4770 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:4776 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:4899 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:4929 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:4935 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:5008 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:5014 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:27739 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:27745 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:28704 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:28722 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:28728 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:28734 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:28740 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:28746 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:28752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:28758 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:28824 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:28960 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:28978 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:28984 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:29080 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:29200 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:29206 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:29212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:29322 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
L:29467 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:29473 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:29479 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:29485 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:29663 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:29669 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:29675 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:29681 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:29839 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:29845 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:29851 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:29857 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:29863 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50

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VERIFICATION SUMMARY DATE: 11/20/2000
PATENT APPLICATION: US/09/373,658A TIME: 16:02:58

Input Set : A:\seqlist14881070006.txt
Output Set: N:\CRF3\11202000\I373658A.raw

L:30189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:30207 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:37476 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:94
L:37476 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:94
L:37476 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:94
L:37476 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:94
L:37476 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:94
L:37494 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:37656 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:98
L:37656 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:98
L:37656 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:98
L:37656 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:98
L:37656 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:98
L:37665 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:98
L:37665 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:98
L:37665 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:98
L:37665 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:98
M:340 Repeated in SeqNo=98
L:37746 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:100
L:37746 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:100
L:37746 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:100
L:37746 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:100
L:37746 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:100
L:37788 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:101
L:37788 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:101
L:37788 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:101
L:37788 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:101
L:37788 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:101
L:37824 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:102
L:37824 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:102
L:37824 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:102
L:37824 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:102
L:37824 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:102
L:37827 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:102
L:37827 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:102
L:37827 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:102
L:37827 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:102
M:340 Repeated in SeqNo=102
L:38208 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:111
L:38208 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:111
L:38208 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:111
L:38208 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:111
L:38208 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:111
L:38220 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:111
L:38220 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:111
L:38220 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:111
L:38220 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:111
M:340 Repeated in SeqNo=111
L:38325 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:114

VERIFICATION SUMMARY DATE: 11/20/2000
PATENT APPLICATION: US/09/373,658A TIME: 16:02:58

Input Set : A:\seqlist14881070006.txt
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L:38325 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:114
L:38325 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:114
L:38325 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:114
L:38325 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:114
L:38328 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:114
L:38328 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:114
L:38328 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:114
L:38328 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:114
M:340 Repeated in SeqNo=114
L:38334 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:114
L:38334 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:114
L:38334 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:114
L:38334 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:114
L:38337 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:114
L:38337 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:114
L:38466 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:117
M:340 Repeated in SeqNo=117
L:38514 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:118
L:38538 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:119
M:340 Repeated in SeqNo=119
L:38622 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:121
L:38703 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:123
M:340 Repeated in SeqNo=123
L:38769 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:124